AMENDMENTS

Amendments to the Specification

1. Please replace the paragraph 113 with the one below:

   In one embodiment, the leucine-based motif is xDxxxLL (SEQ ID NO: 17), wherein x can be any amino acids. In another embodiment, the leucine-based motif is xExxxLL (SEQ ID NO: 18), wherein E is glutamic acid. In another embodiment, the duplet of amino acids can include an isoleucine or a methionine, forming xDxxxLI (SEQ ID NO: 19) or xDxxxLM (SEQ ID NO: 20), respectively. Additionally, the aspartic acid, D, can be replaced by a glutamic acid, E, to form xExxxLI (SEQ ID NO: 21), xExxxIL (SEQ ID NO: 22) and xExxxLM (SEQ ID NO: 23). In a preferred embodiment, the leucine-based motif is phenylalanine-glutamate-phenylalanine-tyrosine-lysine-leucine-leucine, ~~SEQID #1~~ SEQ ID NO: 1.

2. Please replace the paragraph 140 with the one below:

   Tyrosine-based motifs are within the scope of the present invention as biological persistence and/or a biological activity altering components. Tyrosine-based motifs comprise the sequence Y-X-X-Hy (SEQ ID NO: 24), where Y is tyrosine, X is any amino acid and Hy is a hydrophobic amino acid. Tyrosine-based motifs can act in a manner that is similar to that of leucine-based motifs. In figure 3 some of tyrosine motifs found in the type A toxin light chain are bracketed. In addition, a tyrosine-based motif is found within the leucine-based motif which is indicated by an asterisked bracket in figure 3.

3. Please replace the paragraph 143 with the one below:

   Figure 8 shows a sequence alignment between type A and type B light chains isolated from strains type A HallA (~~SEQ ID NO: 19~~ SEQ ID NO: 29) and type B Danish I (~~SEQ ID NO: 20~~ SEQ ID NO: 30) respectively. Light chains or heavy chains isolated from other strains of botulinum toxin types A and B can also be used for sequence comparison.

The shaded amino acids represent amino acid identities, or matches, between the chains. Each of the shaded amino acids between amino acid position 10 and amino acid position 425 of the figure 8 consensus sequence, alone or in combination with any other shaded amino acid or amino acids, represents a biological persistence altering component that is within the scope of the present invention. For example, amino acids KAFK at positions 19 to 22, LNK at positions 304 to 306, L at position 228 in combination with KL at positions 95 and 96, FDKLYK at positions 346 to 351, YL-T at positions 78 to 81, YYD at positions 73 to 75 in combination with YL at positions 78 and 79 in combination with T a position 81, F at position 297 in combination with I at position 300 in combination with KL at positions 95 and 96 can be biological persistence altering components for use within the scope of this invention. In addition, conserved regions of charge, hydrophobicity, hydro-philicity and/or conserved secondary, tertiary, or quaternary structures that may be independent of conserved sequence are within the scope of the present invention.